

IN THE CLAIMS:

These claims will replace all prior versions of claims in the present application.

1. (Previously Presented) A method for judging an eligibility, for array design, of an array including an alkali in a genome array, the method characterized by comprising the steps of:

calculating incidences of partial arrays with a predetermined length in the genome array; and

storing the incidences relating to the partial arrays with the predetermined length in an incidence table.

2. (Original) A method according to Claim 1, characterized by that the step of storing in the incidence table has the steps of:

omitting the storage into the incidence table for partial arrays with the incidence of zero (0); and

using second partial arrays having a shorter second predetermined length than the predetermined length and storing in a second table a position in the incidence table of the partial arrays with the predetermined length including the second partial array from the beginning.

3. (Previously Presented) A method for judging an eligibility, for array design, of an array including an alkali in a genome array, the method characterized by comprising the steps of:

calculating an isolation degree i by which j mutation(s) ($j=1,2, \dots, i-1$) referring to the conversion of j alkali(s) of each of partial arrays with a predetermined length do/does not

appear in the genome array but i mutation(s) referring to the conversion of i alkalis appear(s) in the genome array; and

storing in an isolation degree table the isolation degree with respect to the partial arrays with the predetermined length.

4. (Original) A method according to Claim 3, characterized by that the step for calculating the isolation degree has the steps of:

judging whether or not k mutation(s) referring to the conversion of k alkali(s) of the partial array with the predetermined length exist(s) in the partial array with the predetermined length with reference to an incidence table storing an incidence in a genome array with respect to each of the partial arrays with the predetermined length;

when the k mutation(s) exist(s), determining k as an isolation degree;

when the k mutation(s) does/do not exist, incrementing k and repeating the step of judging the presence of the k mutation(s).

5. (Currently Amended) A method according to Claim 3 or 4 characterized by that the step of calculating the isolation degree has the steps of:

judging, by using second partial arrays having a shorter second predetermined length than the predetermined length and with reference to a second table storing a position, in the incidence table, of the partial arrays with the predetermined length including the second partial array from the beginning, whether the k mutation(s) with the predetermined length exist(s) in which k alkali(s) at a position away from the beginning of the partial array with the predetermined length by a second predetermined length is/are converted;

when the k mutation(s) exist(s), finding a hamming distance between the k mutation(s) and the array with the predetermined length;

when the minimum value of the hamming distance is k, determining the k as an isolation degree thereof;

when the minimum value is larger than k, repeating the step of incrementing k and judging by using the presence of the k mutation(s) with the predetermined length and the minimum value of the hamming distance.

6. (Currently Amended) A method according to Claim 3-~~or~~4, characterized by comprising the step of judging the appearance in the genome array based on whether the incidence in the genome array is equal to or lower than n.

7. (Previously Presented) A method for judging an eligibility for array design of an array including an alkali in a genome array, the method characterized by comprising the steps of:

calculating a shortest partial array by which a partial array starting from the k^{th} letter of a partial array with a predetermined length no longer appears in a genome array; and

calculating the maximum number m of partial array uniquely included in the partial array and handling the m as an indicator indicating an isolation degree thereof by considering the m as the lower bounds of the isolation degree.

8. (Original) A method according to Claim 7, characterized by comprising the step of performing the step of judging whether the partial array appears or not based on whether the incidence in the genome array is equal to or lower than n.

9. (Currently Amended) A method for judging an eligibility, for array design, of an array including an alkali in a genome array, the method characterized by comprising the steps of:

creating an incidence table by using a method according to Claim 1-~~or~~2;

identifying a same number of arrays including the alkali as a predetermined length with respect to each of alkalis included in a genome array;

identifying an incidence relating to each of the identified arrays with reference to the incidence table; and

calculating the first indicator based on a total sum of the identified incidences.

10. (Currently Amended) A method for judging an eligibility, for array design, of an array including an alkali in a genome array, the method characterized by comprising the steps of:

using an isolation degree table created by using a method according to ~~any one of Claims 3 to 8~~ Claim 3;

identifying a same number of arrays including the alkali as a predetermined length with respect to each of alkalis included in a genome array;

identifying an isolation degree relating to each of the identified arrays with reference to the isolation degree table; and

calculating the second indicator based on a total sum of the identified isolation degrees.

11. (Currently Amended) A method for judging an eligibility, for array design, of an array including an alkali in a genome array, characterized by comprising the steps of:

~~using~~ providing an incidence table created by using a first method ~~according to Claim 1 or 2~~

comprising the steps of:

(a) calculating incidences of partial arrays with a predetermined length in the genome array; and

(b) storing the incidences relating to the partial arrays with the predetermined length in an incidence table;

~~using~~ providing an isolation degree table created by using a ~~method according to any one of Claims 3 to 8~~

a second method comprising the steps of:

(a) calculating an isolation degree i by which j mutation(s) ($j=1,2, \dots, i-1$) referring to the conversion of j alkali(s) of each of partial arrays with a predetermined length do/does not appear in the genome array but i mutation(s) referring to the conversion of i alkalis appear(s) in the genome array; and

(b) storing in an isolation degree table the isolation degree with respect to the partial arrays with the predetermined length;

identifying a same number of arrays including the alkali as a predetermined length with respect to each of the alkalis included in a genome array;

identifying an incidence relating to each of the identified arrays with reference to the incidence table;

calculating a first indicator based on a total sum of the identified incidences;

identifying an isolation degree relating to each of the identified arrays with reference to the isolation degree table; and

calculating a second indicator based on a total sum of the identified isolation degrees.

12. (Currently Amended) A method according to ~~any one of Claims 9 to 11~~ Claim 9 characterized by further comprising the steps of:

assigning, based on an calculated indicator, a different display form in accordance with a value or range of the indicator; and

creating an image representing each alkali in a genome array in accordance the assigned display form.

13. (Original) A method according to Claim 12, characterized by that the display form is a color.

14. (Previously Presented) A program for operating a computer for judging an eligibility for array design of an array including an alkali in a genome array and being readable by the computer, the program characterized by causing the computer to perform the steps of:

calculating incidences of partial arrays with a predetermined length in the genome array; and

storing the incidences relating to the partial arrays with the predetermined length in an incidence table.

15. (Original) A program according to Claim 14, characterized by causing the computer to perform the step for storing in the incidence table having the steps of:

omitting the storage into the incidence table for partial arrays with the incidence of zero (0); and

using second partial arrays having a shorter second predetermined length than the predetermined length and storing in a second table a position, in the incidence table, of the

partial arrays with the predetermined length including the second partial array from the beginning.

16. (Previously Presented) A program for operating a computer for judging an eligibility, for array design, of an array including an alkali in a genome array and being readable by the computer, the program characterized by causing the computer to perform the steps of:

calculating an isolation degree i by which j mutation(s) ($j=1,2, \dots, i-1$) referring to the conversion of j alkali(s) of each of partial arrays with a predetermined length do/does not appear in the genome array but i mutation(s) referring to the conversion of i alkalis appear(s) in the genome array; and

storing in an isolation degree table the isolation degree with respect to the partial arrays with the predetermined length.

17. (Original) A program according to Claim 16, characterized by causing the computer to perform the step for calculating the isolation degree having the steps of:

judging whether or not k mutation(s) referring to the conversion of k alkali(s) of the partial array with the predetermined length exist(s) in the partial array with the predetermined length with reference to an incidence table storing an incidence in a genome array with respect to each of the partial arrays with the predetermined length;

when the k mutation(s) exist(s), determining the k as an isolation degree;

when the k mutation(s) does/do not exist, incrementing k and repeating the step of judging the presence of the k mutation(s).

18. (Currently Amended) A program according to Claim 16 ~~or 17~~ characterized by the program causing the computer to perform the step of calculating the isolation degree having the steps of:

judging, by using second partial arrays having a shorter second predetermined length than the predetermined length and with reference to a second table storing a position, in the incidence table, of the partial arrays with the predetermined length including the second partial array from the beginning, whether or not the k mutation(s) with the predetermined length exist(s) in which k alkali(s) at a position away from the beginning of the partial array with the predetermined length by a second predetermined length is/are converted;

when the k mutation(s) exist(s), finding a hamming distance between the k mutation(s) and the array with the predetermined length;

when the minimum value of the hamming distance is k, determining the k as an isolation degree thereof;

when the minimum value is larger than k, repeating the step of incrementing k and judging by using the presence of the k mutation(s) with the predetermined length and the minimum value of the hamming distance.

19. (Currently Amended) A program according to Claim 16 ~~or 17~~, characterized by causing the computer to perform the step of judging the appearance in the genome array based on whether the incidence in the genome array is equal to or lower than n.

20. (Previously Presented) A program for operating a computer for judging an eligibility for array design of an array including an alkali in a genome array and being readable by the computer, the program characterized by causing the computer to perform the steps of:

calculating a shortest partial array by which a partial array starting from the kth letter of a partial array with a predetermined length no longer appears in a genome array; and

calculating the maximum number m of partial array uniquely included in the partial array and handling the m as an indicator indicating an isolation degree thereof by considering the m as the lower bounds of the isolation degree.

21. (Original) A program according to Claim 20, characterized by causing the computer to perform the step of judging whether the partial array appears or not based on whether the incidence in the genome array is equal to or lower than n.

22. (Currently Amended) A computer-readable program for operating a computer for judging an eligibility for array design of an array including an alkali in a genome array and being readable by the computer, the program characterized by causing the computer to perform the steps of:

using an incidence table created by causing the computer to perform a program according to Claim 14 or 15, identifying a same number of arrays including the alkali as a predetermined length with respect to each of alkalis included in a genome array;

identifying an incidence relating to each of the identified arrays with reference to the incidence table; and

calculating a first indicator based on a total sum of the identified incidences.

23. (Currently Amended) A computer-readable program for operating a computer for judging an eligibility, for array design, of an array including an alkali in a genome array and being readable by the computer, the program characterized by causing the computer to perform the steps of:

using an isolation degree table created by causing the computer to perform a program according to ~~any one of Claims 16 to 21~~ Claim 16;

identifying a same number of arrays including the alkali as a predetermined length with respect to each of alkalis included in a genome array;

identifying an isolation degree relating to each of the identified arrays with reference to the isolation degree table; and

calculating the second indicator based on a total sum of the identified isolation degrees.

24. (Currently Amended) A computer-readable program for operating a computer for judging an eligibility, for array design, of an array including an alkali in a genome array and being readable by the computer, the program characterized by causing the computer to perform the steps of:

~~using providing~~ an incidence table created by causing the computer to perform a program according to ~~Claim 14 or 15~~

a program for operating a computer for judging an eligibility for array design of an array including an alkali in a genome array and being readable by the computer, the program characterized by causing the computer to perform the steps of:

(a) calculating incidences of partial arrays with a predetermined length in the genome array; and

(b) storing the incidences relating to the partial arrays with the predetermined length in an incidence table;

~~using providing~~ an isolation degree table created by causing the computer to perform a program according to ~~any one of Claims 16 to 21~~

a program for operating a computer for judging an eligibility, for array design, of an array including an alkali in a genome array and being readable by the computer, the program characterized by causing the computer to perform the steps of:

(a) calculating an isolation degree i by which j mutation(s) ($j=1,2, \dots, i-1$) referring to the conversion of j alkali(s) of each of partial arrays with a predetermined length do/does not appear in the genome array but i mutation(s) referring to the conversion of i alkalis appear(s) in the genome array; and

(b) storing in an isolation degree table the isolation degree with respect to the partial arrays with the predetermined length;

identifying a same number of arrays including the alkali as a predetermined length with respect to each of the alkalis included in a genome array;

identifying an incidence relating to each of the identified arrays with reference to the incidence table;

calculating a first indicator based on a total sum of the identified incidences;

identifying an isolation degree relating to each of the identified arrays with reference to the isolation degree table;

calculating a second indicator based on a total sum of the identified isolation degrees.

25. (Currently Amended) A program according to ~~any one of Claims 22 to 24~~ Claim 22 characterized by further causing the computer to perform the steps of:

assigning, based on an calculated indicator, a different display form in accordance with a value or range of the indicator; and

creating an image representing each alkali in a genome array in accordance the assigned display form.